



#4

## SEQUENCE LISTING

<110> Hauptmann, Rudolph  
Himmler, Adolph  
Maurer-Fogy, Ingrid  
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for  
Them

<130> 98,385-H

<140> 09/899,422  
<141> 2001-07-03

<150> 09/525,998  
<151> 2000-03-15

<150> 08/383,676  
<151> 1995-02-01

<150> 08/153,287  
<151> 1993-11-17

<150> 07/821,750  
<151> 1992-01-02

<150> 07/511,430  
<151> 1990-04-20

<160> 87

<170> PatentIn Ver. 2.0

<210> 1  
<211> 1368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(1368)

<220>  
<221> sig\_peptide  
<222> (1)..(87)

<220>  
<221> misc\_feature  
<222> (88)..(120)  
<223> Portion of TNF-BP pro protein cleaved by  
extracellular proteases following secretion.

<220>  
<221> misc\_feature  
<222> (606)..(633)  
<223> Portion of TNF-BP pro protein cleaved by

extracellular proteases following secretion.

<400> 1

|   |     |
|---|-----|
| atg ggc ctc tcc acc gtg cct gac ctg ctg ctg cca ctg gtg ctc ctg | 48  |
| Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu |     |
| 1 5 10 15   |     |
| gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct | 96  |
| Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro |     |
| 20 25 30  |     |
| cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa | 144 |
| His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys |     |
| 35 40 45  |     |
| tat atc cac cct caa aat aat tgc att tgc tgt acc aag tgc cac aaa | 192 |
| Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys |     |
| 50 55 60  |     |
| gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac | 240 |
| Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp |     |
| 65 70 75 80   |     |
| tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc | 288 |
| Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu |     |
| 85 90 95  |     |
| aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg | 336 |
| Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val |     |
| 100 105 110   |     |
| gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg | 384 |
| Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg |     |
| 115 120 125   |     |
| aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc | 432 |
| Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe |     |
| 130 135 140   |     |
| aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag | 480 |
| Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu |     |
| 145 150 155 160   |     |
| aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa | 528 |
| Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu |     |
| 165 170 175   |     |
| aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg | 576 |
| Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr |     |
| 180 185 190   |     |
| aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca | 624 |
| Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser |     |
| 195 200 205   |     |
| ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt | 672 |
| Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu |     |

| 210   | 215 | 220 |      |
|---|-----|-----|------|
| tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag |     |     | 720  |
| Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys |     |     |      |
| 225   | 230 | 235 | 240  |
| tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag |     |     | 768  |
| Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu |     |     |      |
|   | 245 | 250 | 255  |
| ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc |     |     | 816  |
| Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser |     |     |      |
|   | 260 | 265 | 270  |
| ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg |     |     | 864  |
| Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val |     |     |      |
|   | 275 | 280 | 285  |
| ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt |     |     | 912  |
| Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys |     |     |      |
|   | 290 | 295 | 300  |
| ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg |     |     | 960  |
| Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly |     |     |      |
| 305   | 310 | 315 | 320  |
| gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac |     |     | 1008 |
| Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn |     |     |      |
|   | 325 | 330 | 335  |
| ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac |     |     | 1056 |
| Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp |     |     |      |
|   | 340 | 345 | 350  |
| act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg |     |     | 1104 |
| Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro |     |     |      |
|   | 355 | 360 | 365  |
| ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag |     |     | 1152 |
| Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu |     |     |      |
|   | 370 | 375 | 380  |
| atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa |     |     | 1200 |
| Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln |     |     |      |
| 385   | 390 | 395 | 400  |
| tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc |     |     | 1248 |
| Tyr Ser Met Leu Ala Thr Trp Arg Arg Thr Pro Arg Arg Glu Ala     |     |     |      |
|   | 405 | 410 | 415  |
| acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc |     |     | 1296 |
| Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly |     |     |      |
|   | 420 | 425 | 430  |
| tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg |     |     | 1344 |
| Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro |     |     |      |
|   | 435 | 440 | 445  |

ccc gcg ccc agt ctt ctc aga tga  
 Pro Ala Pro Ser Leu Leu Arg  
 450 455

1368

<210> 2  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30  
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110  
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125  
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140  
 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160  
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175  
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190  
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205  
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220  
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245 250 255  
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260 265 270  
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 275 280 285  
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300  
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
 305 310 315 320  
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
 325 330 335  
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
 340 345 350  
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
 355 360 365  
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
 370 375 380  
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
 385 390 395 400  
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
 405 410 415  
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
 420 425 430  
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
 435 440 445  
 Pro Ala Pro Ser Leu Leu Arg  
 450 455

<210> 3  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(483)

<400> 3  
 gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat tcg 48  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser  
 1 5 10 15

|   |     |
|---|-----|
| att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt | 96  |
| Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys |     |
| 20 25 30  |     |
|   |     |
| cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc | 144 |
| Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser |     |
| 35 40 45  |     |
|   |     |
| ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa | 192 |
| Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys |     |
| 50 55 60  |     |
|   |     |
| tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac | 240 |
| Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp |     |
| 65 70 75 80   |     |
|   |     |
| cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg | 288 |
| Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp |     |
| 85 90 95  |     |
|   |     |
| agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg | 336 |
| Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly |     |
| 100 105 110   |     |
|   |     |
| acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc | 384 |
| Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys |     |
| 115 120 125   |     |
|   |     |
| cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac | 432 |
| His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn |     |
| 130 135 140   |     |
|   |     |
| tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag | 480 |
| Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu |     |
| 145 150 155 160   |     |
|   |     |
| aat   | 483 |
| Asn   |     |

<210> 4  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser  
 1 5 10 15  
 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
 20 25 30  
 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
 35 40 45  
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
 50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
 65 70 75 80  
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
 85 90 95  
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
 100 105 110  
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
 115 120 125  
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
 130 135 140  
 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
 145 150 155 160  
 Asn

<210> 5  
 <211> 87  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(87)

<400> 5  
 atg ggc ctc tcc acc gtg cct gac ctg ctg ctg cca ctg gtg ctc ctg 48  
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
 20 25

<210> 6  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
 20 25

<210> 7  
 <211> 33

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(33)

<400> 7  
ctg gtc cct cac cta ggg gac agg gag aag aga  
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

33

<210> 8  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 8  
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

<210> 9  
<211> 30  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(30)

<400> 9  
gtt aag ggc act gag gac tca ggc acc aca  
Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
1 5 10

30

<210> 10  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 10  
Val Lys Gly Thr Glu Asp Ser Gly Thr Thr  
1 5 10

<210> 11  
<211> 1334  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (213)..(1325)



<220>

<223> Description of Artificial Sequence: cDNA insert of  
lambdaTNF-BP15 and pTNF-BP15 vectors

<400> 11

```
gaattctctg gactgaggct ccagttcttg cctttggggt tcaagatcac tgggaccagg 60
ccgtgatctc tatgcccagag tctcaacctt caactgtcac cccaaggcac ttgggacgtc 120
ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180
aatgggcgag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233
                               Met Gly Leu Ser Thr Val Pro
                               1                               5

gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281
Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
      10                               15                               20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
      25                               30                               35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
      40                               45                               50                               55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
      60                               65                               70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
      75                               80                               85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
      90                               95                               100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
      105                               110                               115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
      120                               125                               130                               135

tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 665
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
      140                               145                               150

ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 713
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr
      155                               160                               165

tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt 761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser
```

| 170   | 175 | 180 |      |
|---|-----|-----|------|
| aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att |     |     | 809  |
| Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile |     |     |      |
| 185   | 190 | 195 |      |
| gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc |     |     | 857  |
| Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro |     |     |      |
| 200   | 205 | 210 | 215  |
| ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt |     |     | 905  |
| Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly |     |     |      |
|   | 220 | 225 | 230  |
| tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt |     |     | 953  |
| Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val |     |     |      |
|   | 235 | 240 | 245  |
| tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act |     |     | 1001 |
| Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr |     |     |      |
| 250   | 255 | 260 |      |
| act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc |     |     | 1049 |
| Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe |     |     |      |
| 265   | 270 | 275 |      |
| acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc |     |     | 1097 |
| Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser |     |     |      |
| 280   | 285 | 290 | 295  |
| agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc |     |     | 1145 |
| Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg |     |     |      |
|   | 300 | 305 | 310  |
| aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca |     |     | 1193 |
| Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr |     |     |      |
|   | 315 | 320 | 325  |
| gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac |     |     | 1241 |
| Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp |     |     |      |
| 330   | 335 | 340 |      |
| agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg |     |     | 1289 |
| Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu |     |     |      |
| 345   | 350 | 355 |      |
| tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggaattc       |     |     | 1334 |
| Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp                 |     |     |      |
| 360   | 365 | 370 |      |

<210> 12

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA insert of  
lambdaTNF-BP15 and pTNF-BP15 vectors

<400> 12

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Ser | Thr | Val | Pro | Asp | Leu | Leu | Leu | Pro | Leu | Val | Leu | Leu | 1   | 5   | 10  | 15  |
| Glu | Leu | Leu | Val | Gly | Ile | Tyr | Pro | Ser | Gly | Val | Ile | Gly | Leu | Val | Pro | 20  | 25  | 30  |     |
| His | Leu | Gly | Asp | Arg | Glu | Lys | Arg | Asp | Ser | Val | Cys | Pro | Gln | Gly | Lys | 35  | 40  | 45  |     |
| Tyr | Ile | His | Pro | Gln | Asn | Asn | Ser | Ile | Cys | Cys | Thr | Lys | Cys | His | Lys | 50  | 55  | 60  |     |
| Gly | Thr | Tyr | Leu | Tyr | Asn | Asp | Cys | Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp | 65  | 70  | 75  | 80  |
| Cys | Arg | Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | 85  | 90  | 95  |     |
| Arg | His | Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | 100 | 105 | 110 |     |
| Glu | Ile | Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | 115 | 120 | 125 |     |
| Lys | Asn | Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | 130 | 135 | 140 |     |
| Asn | Cys | Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | 145 | 150 | 155 | 160 |
| Lys | Gln | Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | 165 | 170 | 175 |     |
| Asn | Glu | Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr | 180 | 185 | 190 |     |
| Lys | Leu | Cys | Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser | 195 | 200 | 205 |     |
| Gly | Thr | Thr | Val | Leu | Leu | Pro | Leu | Val | Ile | Phe | Phe | Gly | Leu | Cys | Leu | 210 | 215 | 220 |     |
| Leu | Ser | Leu | Leu | Phe | Ile | Gly | Leu | Met | Tyr | Arg | Tyr | Gln | Arg | Trp | Lys | 225 | 230 | 235 | 240 |
| Ser | Lys | Leu | Tyr | Ser | Ile | Val | Cys | Gly | Lys | Ser | Thr | Pro | Glu | Lys | Glu | 245 | 250 | 255 |     |
| Gly | Glu | Leu | Glu | Gly | Thr | Thr | Thr | Lys | Pro | Leu | Ala | Pro | Asn | Pro | Ser | 260 | 265 | 270 |     |
| Phe | Ser | Pro | Thr | Pro | Gly | Phe | Thr | Pro | Thr | Leu | Gly | Phe | Ser | Pro | Val | 275 | 280 | 285 |     |

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp  
370

<210> 13  
<211> 6414  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: pADCMV1 vector

<220>  
<221> unsure  
<222> (344)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (4157)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (5135)  
<223> "n" can be a, g, c, or t

<220>  
<221> unsure  
<222> (6255)  
<223> "n" can be a, g, c, or t

<400> 13  
tcgacattga ttattgacta gttattaata gtaatcaatt acggggtcat tagttcatag 60  
cccatatatg gagttccgcg ttacataact tacggtaaatt ggcccgcctc gctgaccgcc 120  
caacgacccc cgccattga cgtcaataat gacgtatggt cccatagtaa cgccaatagg 180  
gactttccat tgacgtcaat ggggtggagta ttacggtaa actgcccact tggcagtaca 240

tcaagtgtat catatgccaa gtacgcccc tattgacgtc aatgacggta aatggccccg 300  
ctggcattat gccagtaga tgacctatg ggactttcct actnggcagt acatctacgt 360  
attagtcac gctattacca tggatgatgc gttttggcag tacatcaatg ggcgtaggata 420  
gcggtttgac tcacggggat ttccaagtct ccacccatt gacgtcaatg ggagtttgtt 480  
ttggcaccaa aatcaacggg actttccaaa atgtcgtaac aactccgcc cattgacgca 540  
aatgggcggg aggcgtgtac ggtgggaggt ctatataagc agagctctct ggctaactag 600  
agaaccact gcttaactgg cttatcgaaa ttaatacgac tcactatagg gagaccaag 660  
cttctgcagg tcgacatcga tggatccgg acctcgagcg cgaattctct agaggatctt 720  
tgtgaaggaa ccttacttct gtggtgtgac ataattggac aaactaccta cagagattta 780  
aagctctaag gtaaataata aatttttaag tgtataatgt gttaaactac tgattctaata 840  
tgtttgtgta ttttagattc caacctatgg aactgatgaa tgggagcagt ggtggaatgc 900  
ctttaatgag gaaaacctgt ttgctcaga agaatgcc aatagtgatg atgaggctac 960  
tgctgactct caacattcta ctctccaaa aaagaagaga aaggtagaag accccaagga 1020  
ctttccttca gaattgctaa gttttttgag tcatgctgtg tttagtaata gaactcttgc 1080  
ttgctttgct atttacacca caaaggaaaa agctgcactg ctatacaaga aaattatgga 1140  
aaaatatttg atgtatagtg ccttgactag agatcataat cagccatacc acatttgtag 1200  
aggttttact tgctttaaaa aacctccac acctccccct gaacctgaaa cataaaatga 1260  
atgcaattgt tgttgtaaac ttgtttattg cagcttataa tggttacaaa taaagcaata 1320  
gcatcacaaa tttcacaaat aaagcatttt tttcactgca ttctagttgt ggtttgtcca 1380  
aactcatcaa tgtatcttat catgtctgga tcaattctga gaaactagcc ttaaagacag 1440  
acagctttgt tctagtcagc caggcaagca tatgtaaata aagttcctca gggaactgag 1500  
gttaaaagat gtatcctgga cctgccagac ctggccattc acgtaaacag aagattccgc 1560  
ctcaagttcc ggttaacaac aggaggcaac gagatctcaa atctattact tctaactggg 1620  
taattaaaac ctttcaacta aaacacggac ccacggatgt caccacttt tccttccccg 1680  
gctccgccct tctcagtact cccaccatt aggcctgcta ctccacctcc acttccgggc 1740  
gcgacacca cgtgccctct ccacccgac gctaaccocg ccctgcccg tctgaccccg 1800  
cccaccact ggccccgcc cgttgaggac agaagaaacc ccgggcagcc gcagccaagg 1860  
cggacgggta gacgtgggg gcgctgagga gtcgtctct accttctctg ctggctcggt 1920  
gggggacgcg gtggatctca ggcttccgga agactggaag aaccggctca gaaccgctt 1980

tctccgcggg gcttgggcgg cggaagaatg gccgctagac gccgacttgg tgcgagggcat 2040  
cgcaggatgc agaagagcaa gcccgccggg agcgcgcggc tgtactaccc cgcgcctgga 2100  
gcggccacgc cggactgggc ggggcccggc tgggtggaggc ggagtctgac ctctggagg 2160  
cggggcctct gatgttcaaa taggatgcta ggcttgttga ggctggcct ccgattcaca 2220  
agtgggaagc agcgccgggc gactgcaatt tcgcgcaaaa cttgggggaa gcacagcgta 2280  
caggctgcct aggtgatcgc tgctgctgtc atggttcgac cgctgaactg catcgtcgcc 2340  
gtgtcccaga atatgggcat cggcaagaac ggagaccttc cctggccaat gctcagggtac 2400  
tggttgatt gggttaggga aaccgaggcg gttcgctgaa tcgggtcgag cacttggcgg 2460  
agacgcgcgg gccaaactact tagggacagt catgaggggt agggccgcgc gctgctgccc 2520  
ttgcccatgc ccgcggtgat ccccatgctg tgccagcctt tgcccagagg cgctctagct 2580  
gggagcaaag tccggtcact gggcagcacc acccccggga cttgcatggg tagccgctga 2640  
gatggagcct gagcacacgt gacagggtcc ctgttaacgc agtgtttctc taactttcag 2700  
gaacgagttc aagtacttcc aaagaatgac caccacctcc tcagtgaag gtaaacagaa 2760  
cctggtgatt atgggccgga aaacctggtt ctccattcct gagaagaatc gacctttaa 2820  
ggacagaatt aatatagttc tcagtagaga gctcaaggaa ccaccacaag gagctcattt 2880  
tcttgccaaa agtctggacc atgccttaaa acttattgaa caaccagagt tagcagataa 2940  
agtggacatg gtttgatag ttggaggcag ttccgtttac aaggaagcca tgaatcagcc 3000  
aggccatctc agactctttg tgacaaggat catgcaggaa ttgaaagtg acacgttctt 3060  
cccagaaatt gatttgaga aatataaact tctcccagag taccagggg tctttctga 3120  
agtccaggag gaaaaaggca tcaagtataa atttgaagtc tatgagaaga aaggctaaca 3180  
gaaagatact tgctgattga cttcaagttc tactgctttc ctctaaaat tatgcatttt 3240  
tacaagacca tgggacttgt gttggcttta gatcctgtgc atcctgggca actgttgtac 3300  
tctaagccac tccccaaagt catgccccag ccctgtata attctaaaca attagaatta 3360  
ttttcatttt cattagtcta accaggttat attaaatata ctttaagaaa caccatttgc 3420  
cataaagttc tcaatgcccc tcccatgcag cctcaagtgg ctccccagca gatgcatagg 3480  
gtagtgtgtg tacaagagac cccaaagaca tagagcccct gagagcatga gctgatatgg 3540  
gggctcatag agataggagc tagatgaata agtacaaagg gcagaaatgg gttttaacca 3600  
gcagagctag aactcagact ttaaagaaaa ttagatcaaa gtagagactg aattattctg 3660

cacatcagac tctgagcaga gttctgttca ctacagacaga aaatgggtaa attgagagct 3720  
ggctccattg tgctccttag agatgggagc aggtggagga ttatataagg tctggaacat 3780  
ttaactttctc cgttttctcat cttcagtgag attccaaggg atactacaat tctgtggaat 3840  
gtgtgtcagt taggggtgtg aaagtcccca ggctccccag caggcagaag tatgcaaagc 3900  
atgcatctca attagtcagc aaccaggtgt ggaaagtccc caggctcccc agcaggcaga 3960  
agtatgcaaa gcatgcatct caattagtcg gcaaccatag tcccgcccct aactccgccc 4020  
atcccgcccc taactccgcc cagttccgcc cattctccgc cccatggctg actaattttt 4080  
tttattttatg cagaggccga ggcgccctctg agctattcca gaagtagtga ggaggctttt 4140  
ttggaggcct aggccttntgc aaaaaagcta attcagcctg aatggcgaat gggacgcgcc 4200  
ctgtagcggc gcattaagcg cggcggtgt ggtggttaag cgcagcgtga ccgctacact 4260  
tgccagcgcc ctacgcgccg ctcccttccg tttcttccct tcccttctcg ccacgttccg 4320  
cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat ttagtgcttt 4380  
acggcacctc gacccccaaa acttgattag ggtgatggtt cacgtagtgg gccatcgccc 4440  
tgatagacgg tttttcgccc tttagcgttg gagtccacgt tctttaatag tggactcttg 4500  
ttccaaactg gaacaacact caaccctatc tcggtctatt cttttgattt ataagggatt 4560  
ttgccgattt cggcctattg gttaaaaaat gagctgattt aacaaaaatt taacgcgaat 4620  
tttaacaaaa tattaacgtt tacaatttca ggtggcactt ttcggggaaa tgtgcgcgga 4680  
accctatatt gtttattttt ctaaatacat tcaaataatgt atccgctcat gagacaataa 4740  
ccctgataaa tgcttcaata atattgaaaa aggaagagta tgagtattca acatttccgt 4800  
gtcgccctta ttcccttttt tgccggcattt tgccttccctg tttttgctca cccagaaacg 4860  
ctggtgaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggtta catcgaactg 4920  
gatctcaaca gcggttaagat ccttgagagt tttagccccc aagaacgttt tccaatgatg 4980  
agcactttta aagttctgct atgtggcgcg gtattatccc gtattgacgc cgggcaagag 5040  
caactcggtc gccgcataca ctattctcag aatgacttgg ttgagtactc accagtcaca 5100  
gaaaagcatc ttacggatgg catgacagta agagnattat gcagtgtctc cataaccatg 5160  
agtataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa ggagctaacc 5220  
gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga accggagctg 5280  
aatgaagcca tacāaaacga cgagcgtgac accacgatgc ctgtagcaat ggcaacaacg 5340  
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 5400

tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 5460  
 tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 5520  
 gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 5580  
 atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattggtaa 5640  
 ctgtcagacc aagtttactc atatatactt tagattgatt taaaacttca tttttaattt 5700  
 aaaaggatct aggtgaagat cctttttgat aatctcatga ccaaaatccc ttaacgtgag 5760  
 ttttcgttcc actgagcgtc agaccccgta gaaaagatca aaggatcttc ttgagatcct 5820  
 ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac caccgctacc agcgggtggtt 5880  
 tgtttgccgg atcaagagct accaactctt tttccgaagg taactggctt cagcagagcg 5940  
 cagataccaa atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct 6000  
 gtagcaccgc ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc 6060  
 gataagtcgt gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg 6120  
 tcgggctgaa cgggggggtc gtgcacacag ccagcttgg agcgaacgac ctacaccgaa 6180  
 ctgagatacc tacagcgtga gcattgagaa agcgccacgc ttcccgaagg gagaaaggcg 6240  
 gacaggtatc cggtnagcgg cagggtcgga acaggagagc gcacgaggga gcttccaggg 6300  
 ggaaacgcct ggtatcttta tagtcctgtc ggggttcgcc acctctgact tgagcgtcga 6360  
 tttttgtgat gctcgtcagg ggggcgagc ctatggaaaa acgccagcaa cgcc 6414

<210> 14

<211> 2173

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (245)..(1630)

<220>

<223> Description of Artificial Sequence: raTNF-R8

<400> 14

gaattccttt tctccgagtt ttctgaactc tggctcatga tcgggcttac tggatacgag 60  
 aatcctggag gaccgtaccc tgatttccat ctacctctga ctttgagcct ttctaaccgg 120  
 gggctcacgc tgccaacacc cgggccacct ggtccgatcg tcttacttca ttcaccagcg 180  
 ttgccaattg ctgcctgtc cccagcccca atgggggagt gagagaggcc actgccggcc 240



|  |     |
|--|-----|
| ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc | 289 |
| Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu      |     |
| 1 5 10 15  |     |
| ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt  | 337 |
| Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val  |     |
| 20 25 30   |     |
| cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga  | 385 |
| Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly  |     |
| 35 40 45   |     |
| aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac  | 433 |
| Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His  |     |
| 50 55 60   |     |
| aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca  | 481 |
| Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr  |     |
| 65 70 75   |     |
| gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac  | 529 |
| Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His  |     |
| 80 85 90 95  |     |
| gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag  | 577 |
| Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln  |     |
| 100 105 110  |     |
| gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc  | 625 |
| Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys  |     |
| 115 120 125  |     |
| aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt  | 673 |
| Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys  |     |
| 130 135 140  |     |
| gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag  | 721 |
| Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys  |     |
| 145 150 155  |     |
| gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc  | 769 |
| Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser  |     |
| 160 165 170 175  |     |
| gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt  | 817 |
| Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys  |     |
| 180 185 190  |     |
| atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac  | 865 |
| Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp  |     |
| 195 200 205  |     |
| tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt ctt tgc  | 913 |
| Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys  |     |
| 210 215 220  |     |
| ctt tta ttc ttt atc tgc atc agt cta ctg tgc cga tat ccc cag tgg  | 961 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Leu | Leu | Phe | Phe | Ile | Cys | Ile | Ser | Leu | Leu | Cys | Arg | Tyr | Pro | Gln | Trp |      |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |      |
| agg | ccc | agg | gtc | tac | tcc | atc | att | tgt | agg | gat | tca | gct | cct | gtc | aaa | 1009 |
| Arg | Pro | Arg | Val | Tyr | Ser | Ile | Ile | Cys | Arg | Asp | Ser | Ala | Pro | Val | Lys |      |
| 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |      |
| gag | gtg | gag | ggg | gaa | gga | att | gtt | act | aag | ccc | cta | act | cca | gcc | tct | 1057 |
| Glu | Val | Glu | Gly | Glu | Gly | Ile | Val | Thr | Lys | Pro | Leu | Thr | Pro | Ala | Ser |      |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |      |
| atc | cca | gcc | ttc | agc | ccc | aac | ccc | ggc | ttc | aac | ccc | act | ctg | ggc | ttc | 1105 |
| Ile | Pro | Ala | Phe | Ser | Pro | Asn | Pro | Gly | Phe | Asn | Pro | Thr | Leu | Gly | Phe |      |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |      |
| agc | acc | acc | cca | cgc | ttc | agt | cat | cct | gtc | tcc | agt | acc | ccc | atc | agc | 1153 |
| Ser | Thr | Thr | Pro | Arg | Phe | Ser | His | Pro | Val | Ser | Ser | Thr | Pro | Ile | Ser |      |
|     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |      |
| ccc | gtc | ttc | ggg | cct | agt | aac | tgg | cac | aac | ttc | gtg | cca | cct | gta | aga | 1201 |
| Pro | Val | Phe | Gly | Pro | Ser | Asn | Trp | His | Asn | Phe | Val | Pro | Pro | Val | Arg |      |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |      |
| gag | gtg | gtc | cca | acc | cag | ggg | gct | gac | cct | ctc | ctc | tac | gga | tcc | ctc | 1249 |
| Glu | Val | Val | Pro | Thr | Gln | Gly | Ala | Asp | Pro | Leu | Leu | Tyr | Gly | Ser | Leu |      |
| 320 |     |     |     |     | 325 |     |     |     | 330 |     |     |     |     | 335 |     |      |
| aac | cct | gtg | cca | atc | ccc | gcc | cct | gtt | cgg | aaa | tgg | gaa | gac | gtc | gtc | 1297 |
| Asn | Pro | Val | Pro | Ile | Pro | Ala | Pro | Val | Arg | Lys | Trp | Glu | Asp | Val | Val |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |      |
| gcg | gcc | cag | cca | caa | cgg | ctt | gac | act | gca | gac | cct | gcg | atg | ctg | tat | 1345 |
| Ala | Ala | Gln | Pro | Gln | Arg | Leu | Asp | Thr | Ala | Asp | Pro | Ala | Met | Leu | Tyr |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| gct | gtg | gtg | gat | ggc | gtg | cct | ccg | aca | cgc | tgg | aag | gag | ttc | atg | cgg | 1393 |
| Ala | Val | Val | Asp | Gly | Val | Pro | Pro | Thr | Arg | Trp | Lys | Glu | Phe | Met | Arg |      |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| ctc | ctg | ggg | ctg | agc | gag | cac | gag | atc | gag | cgg | ttg | gag | ctg | cag | aac | 1441 |
| Leu | Leu | Gly | Leu | Ser | Glu | His | Glu | Ile | Glu | Arg | Leu | Glu | Leu | Gln | Asn |      |
|     | 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     |      |
| ggg | cgt | tgc | ctc | cgc | gag | gct | cat | tac | agc | atg | ctg | gaa | gcc | tgg | cgg | 1489 |
| Gly | Arg | Cys | Leu | Arg | Glu | Ala | His | Tyr | Ser | Met | Leu | Glu | Ala | Trp | Arg |      |
| 400 |     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |      |
| cgc | cgc | aca | ccg | cga | cac | gag | gcc | acg | ctg | gac | gta | gtg | ggc | cgc | gtg | 1537 |
| Arg | Arg | Thr | Pro | Arg | His | Glu | Ala | Thr | Leu | Asp | Val | Val | Gly | Arg | Val |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |      |
| ctt | tgc | gac | atg | aac | ctg | cgt | ggc | tgc | ctg | gag | aac | atc | cgc | gag | act | 1585 |
| Leu | Cys | Asp | Met | Asn | Leu | Arg | Gly | Cys | Leu | Glu | Asn | Ile | Arg | Glu | Thr |      |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| cta | gaa | agc | cct | gcc | cac | tcg | tcc | acg | acc | cac | ctc | ccg | cga | taa |     | 1630 |
| Leu | Glu | Ser | Pro | Ala | His | Ser | Ser | Thr | Thr | His | Leu | Pro | Arg |     |     |      |

450

455

460

ggccacaccc ccacctcagg aacgggactc gaaggaccat cctgctagat gccctgcttc 1690  
 cctgtgaacc tcctcttttg tcctctaggg ggcaggctcg atctggcagg ctcgatctgg 1750  
 cagccacttc cttgggtgcta ccgacttggt gtacatagct tttcccagct gccgaggaca 1810  
 gcctgtgcca gccacttggt catggcaggg aagtgtgcca tctgctccca gacagctgag 1870  
 ggtgccaaaa gccaggagag gtgattgtgg agaaaaagca caatctatct gatacccact 1930  
 tgggatgcaa ggacccaaac aaagcttctc agggcctcct cagttgattt ctgggccctt 1990  
 ttcacagtag ataaaacagt ctttgtattg attatatcac actaatggat gaacggttga 2050  
 actccctaag gtaggggcaa gcacagaaca gtgggggtctc cagctggagc ccccgactct 2110  
 tgtaaataca ctaaaaatct aaaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaggaa 2170  
 ttc 2173

&lt;210&gt; 15

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: raTNF-R8

&lt;400&gt; 15

Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu  
 1 5 10 15

Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro  
 20 25 30

Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val  
 65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val  
 85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val  
 100 105 110

Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys  
 115 120 125

Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val

| 130  | 135 | 140 |
|--|-----|-----|
| Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu<br>145 150 155 160 |     |     |
| Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly<br>165 170 175     |     |     |
| Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met<br>180 185 190     |     |     |
| Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser<br>195 200 205     |     |     |
| Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu<br>210 215 220     |     |     |
| Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg<br>225 230 235 240 |     |     |
| Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu<br>245 250 255     |     |     |
| Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile<br>260 265 270     |     |     |
| Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe Ser<br>275 280 285     |     |     |
| Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser Pro<br>290 295 300     |     |     |
| Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu<br>305 310 315 320 |     |     |
| Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn<br>325 330 335     |     |     |
| Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala<br>340 345 350     |     |     |
| Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr Ala<br>355 360 365     |     |     |
| Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg Leu<br>370 375 380     |     |     |
| Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly<br>385 390 395 400 |     |     |
| Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg<br>405 410 415     |     |     |
| Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu<br>420 425 430     |     |     |
| Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu                    |     |     |

435

440

445

Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg  
 450 455 460

&lt;210&gt; 16

&lt;211&gt; 2141

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (213)..(1580)

&lt;220&gt;

<223> Description of Artificial Sequence: human TNF-R in  
 lTNF-R2

&lt;400&gt; 16

gaattctctg gactgaggct ccagttcttg cctttggggt tcaagatcac tgggaccagg 60

ccgtgatctc tatgcccagag tctcaaccct caactgtcac cccaaggcac ttgggacgtc 120

ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180

katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233  
 Met Gly Leu Ser Thr Val Pro  
 1 5

gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281  
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
 10 15 20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
 25 30 35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
 40 45 50 55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
 60 65 70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
 75 80 85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
 90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
 105 110 115

|   |      |
|---|------|
| gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat | 617  |
| Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr |      |
| 120 125 130 135   |      |
| tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat | 665  |
| Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn |      |
| 140 145 150   |      |
| ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc | 713  |
| Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr |      |
| 155 160 165   |      |
| tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt | 761  |
| Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser |      |
| 170 175 180   |      |
| aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att | 809  |
| Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile |      |
| 185 190 195   |      |
| gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc | 857  |
| Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro |      |
| 200 205 210 215   |      |
| ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt | 905  |
| Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly |      |
| 220 225 230   |      |
| tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt | 953  |
| Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val |      |
| 235 240 245   |      |
| tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act | 1001 |
| Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr |      |
| 250 255 260   |      |
| act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc | 1049 |
| Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe |      |
| 265 270 275   |      |
| acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc | 1097 |
| Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser |      |
| 280 285 290 295   |      |
| agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc | 1145 |
| Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg |      |
| 300 305 310   |      |
| aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca | 1193 |
| Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr |      |
| 315 320 325   |      |
| gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac | 1241 |
| Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp |      |
| 330 335 340   |      |

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg 1289  
 Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu  
 345 350 355  
  
 tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aag gaa ttc gtg 1337  
 Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val  
 360 365 370 375  
  
 cgg cgc cta ggg ctg agc gac cac gag atc gat cgg ctg gag ctg cag 1385  
 Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln  
 380 385 390  
  
 aac ggg cgc tgc ctg cgc gag gcg caa tac agc atg ctg gcg acc tgg 1433  
 Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp  
 395 400 405  
  
 agg cgg cgc acg ccg cgg cgc gag gcc acg ctg gag ctg ctg gga cgc 1481  
 Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg  
 410 415 420  
  
 gtg ctc cgc gac atg gac ctg ctg ggc tgc ctg gag gac atc gag gag 1529  
 Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu  
 425 430 435  
  
 gcg ctt tgc ggc ccc gcc gcc ctc ccg ccc gcg ccc agt ctt ctc aga 1577  
 Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg  
 440 445 450 455  
  
 tga ggctgcgccc ctgcgggcag ctctaaggac cgtcctgcga gatcgccttc 1630  
  
 caaccccact tttttctgga aaggaggggt cctgcagggg caagcaggag ctagcagccg 1690  
 cctacttggt gctaaccct cgatgtacat agcttttctc agctgcctgc gcgcgcgcca 1750  
 cagtcagcgc tgtgcgcgcg gagagaggtg cgcctggtgc tcaagagcct gagtgggtgg 1810  
 ttgcgagga tgagggacgc tatgcctcat gcccgttttg ggtgtcctca ccagcaaggc 1870  
 tgctcggggg cccctgggtc gtccctgagc ctttttcaca gtgcataagc agtttttttt 1930  
 gtttttgttt tgttttgttt tgtttttaaa tcaatcatgt tacactaata gaaacttggc 1990  
 actcctgtgc cctctgctg gacaagcaca tagcaagctg aactgtccta aggcaggggc 2050  
 gagcacggaa caatggggcc ttcagctgga gctgtggact ttgtacata cactaaaatt 2110  
 ctgaagttaa aaaaaaaaaa aaaaggaatt c 2141

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in

1TNF-R2

<400> 17

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Ser | Thr | Val | Pro | Asp | Leu | Leu | Leu | Pro | Leu | Val | Leu | Leu | 1   | 5   | 10  | 15  |
| Glu | Leu | Leu | Val | Gly | Ile | Tyr | Pro | Ser | Gly | Val | Ile | Gly | Leu | Val | Pro | 20  | 25  | 30  |     |
| His | Leu | Gly | Asp | Arg | Glu | Lys | Arg | Asp | Ser | Val | Cys | Pro | Gln | Gly | Lys | 35  | 40  | 45  |     |
| Tyr | Ile | His | Pro | Gln | Asn | Asn | Ser | Ile | Cys | Cys | Thr | Lys | Cys | His | Lys | 50  | 55  | 60  |     |
| Gly | Thr | Tyr | Leu | Tyr | Asn | Asp | Cys | Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp | 65  | 70  | 75  | 80  |
| Cys | Arg | Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | 85  | 90  | 95  |     |
| Arg | His | Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | 100 | 105 | 110 |     |
| Glu | Ile | Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | 115 | 120 | 125 |     |
| Lys | Asn | Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | 130 | 135 | 140 |     |
| Asn | Cys | Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | 145 | 150 | 155 | 160 |
| Lys | Gln | Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | 165 | 170 | 175 |     |
| Asn | Glu | Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr | 180 | 185 | 190 |     |
| Lys | Leu | Cys | Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser | 195 | 200 | 205 |     |
| Gly | Thr | Thr | Val | Leu | Leu | Pro | Leu | Val | Ile | Phe | Phe | Gly | Leu | Cys | Leu | 210 | 215 | 220 |     |
| Leu | Ser | Leu | Leu | Phe | Ile | Gly | Leu | Met | Tyr | Arg | Tyr | Gln | Arg | Trp | Lys | 225 | 230 | 235 | 240 |
| Ser | Lys | Leu | Tyr | Ser | Ile | Val | Cys | Gly | Lys | Ser | Thr | Pro | Glu | Lys | Glu | 245 | 250 | 255 |     |
| Gly | Glu | Leu | Glu | Gly | Thr | Thr | Thr | Lys | Pro | Leu | Ala | Pro | Asn | Pro | Ser | 260 | 265 | 270 |     |
| Phe | Ser | Pro | Thr | Pro | Gly | Phe | Thr | Pro | Thr | Leu | Gly | Phe | Ser | Pro | Val | 275 | 280 | 285 |     |



Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300  
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
 305 310 315 320  
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
 325 330 335  
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
 340 345 350  
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
 355 360 365  
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
 370 375 380  
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
 385 390 395 400  
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
 405 410 415  
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
 420 425 430  
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
 435 440 445  
 Pro Ala Pro Ser Leu Leu Arg  
 450 455

<210> 18  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: N-terminal  
 amino acid sequence of protein purified from urine  
 (main sequence)

<220>  
 <221> UNSURE  
 <222> (4)  
 <223> Identity of "Xaa" could not be determined.

<400> 18  
 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln  
 1 5 10

<210> 19  
 <211> 9  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(sudsidiary sequence)

<220>

<221> UNSURE

<222> (7)

<223> Identity of "Xaa" could not be determined.

<400> 19

Leu Val Pro His Leu Gly Xaa Arg Glu  
1 5

<210> 20

<211> 151

<212> DNA

<213> Homo sapiens

<400> 20

caggggaaaa tattcaccct caaataattc gatttgctgt accaagtgcc acaaaggaaa 60  
ctacttgtag aatgactgtc caggcccggg gcaggatacg gactgcaggg agtgtgagag 120  
cggctccttc acagcctcag aaaacaacaa g 151

<210> 21

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 21

Asp Ser Val Cys Pro Gln Gly Lys  
1 5

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (1)..(2)

<223> Identity of "Xaa" could not be determined.

<400> 22  
Xaa Xaa Leu Ser Cys Ser Lys  
1 5

<210> 23  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 23  
Asp Thr Val Cys Gly Cys Arg  
1 5

<210> 24  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 24  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
1 5 10

<210> 25  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 25  
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
1 5 10

<210> 26  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
 <221> UNSURE  
 <222> (6)  
 <223> Identity of "Xaa" could not be determined.

<220>  
 <221> UNSURE  
 <222> (10)..(12)  
 <223> Identity of "Xaa" could not be determined.

<400> 26  
 Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys  
 1 5 10

<210> 27  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
 cleavage peptide

<400> 27  
 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
 1 5 10

<210> 28  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
 cleavage peptide

<400> 28  
 Leu Val Pro His Leu Gly Asp Arg  
 1 5

<210> 29  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
 cleavage peptide

<400> 29  
 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
 1 5 10 15

<210> 30  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 30  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
1 5 10

<210> 31  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
<221> UNSURE  
<222> (9)..(11)  
<223> Identity of "Xaa" could not be determined.

<400> 31  
Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp  
1 5 10

<210> 32  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 32  
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp  
1 5 10 15

Thr Val Cys Gly  
20

<210> 33  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic

cleavage peptide

<220>  
<221> UNSURE  
<222> (6)  
<223> Identity of "Xaa" could not be determined.

<220>  
<221> UNSURE  
<222> (18)  
<223> Identity of "Xaa" could not be determined.

<400> 33  
Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
1 5 10 15

Gly Xaa Tyr

<210> 34  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
<221> UNSURE  
<222> (16)..(17)  
<223> Identity of "Xaa" could not be determined.

<400> 34  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa  
1 5 10 15

Xaa Arg

<210> 35  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 35  
Leu Cys Leu Pro Gln Ile Glu Asn  
1 5

<210> 36

<211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <220>  
 <221> UNSURE  
 <222> (7)  
 <223> Identity of "Xaa" could not be determined.  
  
 <400> 36  
 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg  
   1                  5                  10  
  
  
 <210> 37  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <400> 37  
 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
   1                  5                  10  
  
  
 <210> 38  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <400> 38  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
   1                  5                  10  
  
  
 <210> 39  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <400> 39  
 Gln Gly Lys Tyr Ile His Pro

1

5

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 40  
caaggtaa atattcatcc

20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 41  
cagggtaagt acatccatcc

20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 42  
caaggtaa atatacatcc

20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 43  
caaggcaa atattcatcc

20

<210> 44  
<211> 20



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 44  
 cagggcaagt acatccaccc 20  
  
  
 <210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 45  
 caaggcaa atatacatcc 20  
  
  
 <210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 46  
 caaggaaa atattcatcc 20  
  
  
 <210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 47  
 cagggaaagt acatccaccc 20  
  
  
 <210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization

probe

<400> 48  
caaggaaaat atatacatcc 20

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 49  
caagggaaaat atattcatcc 20

<210> 50  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 50  
caggggaagt acatccaccc 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 51  
caagggaaaat atatacatcc 20

<210> 52  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 52  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 53  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 53  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
1 5 10

<210> 54  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 54  
Phe Thr Ala Ser Glu Asn Asn Lys  
1 5

<210> 55  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 55  
Phe Thr Ala Ser Cys Asn Asn Lys  
1 5

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 56  
aaatgacgga gactcttggt gttcctaggg

30

<210> 57  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 57  
 aagtggcgta gtcttttggt gttcctaggg 30  
  
 <210> 58  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 58  
 aaatgtcgga gactcttggt gttcctaggg 30  
  
 <210> 59  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 59  
 aaatgacggt cactcttggt gttcctaggg 30  
  
 <210> 60  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 60  
 aagtggcggt ctcttttggt gttcctaggg 30  
  
 <210> 61  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 61  
 aaatgtcggg cactcttggt gttcctaggg 30

<210> 62  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 62  
 aaatgacgga gaacattggt gttcctaggg 30

<210> 63  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 63  
 aagtggcgta gtactttggt gttcctaggg 30

<210> 64  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 64  
 aaatgtcgga gaacattggt gttcctaggg 30

<210> 65  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization  
 probe

<400> 65

aaatgacggt caacattggt gttcctaggg

30

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 66

aagtggcggt ctactttggt gttcctaggg

30

<210> 67

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 67

aaatgtcggt caacattggt gttcctaggg

30

<210> 68

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(153)

<400> 68

cag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag 48

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys

1

5

10

15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96

Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln

20

25

30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144

Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu

35

40

45

aac aac aag gatcc

158

Asn Asn Lys

50

<210> 69

<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 69  
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys  
1 5 10 15  
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30  
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45  
Asn Asn Lys  
50

<210> 70  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1786

<400> 70  
ggaattcagc ctgaatggcg aatggg 26

<210> 71  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1729

<400> 71  
cctcgagcgt tgctggcggt tttcc 25

<210> 72  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1733

<400> 72  
ggtcgacatt gattattgac tag 23

<210> 73  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1734

<400> 73  
ggaattcctt aggaatacag cgg

23

<210> 74  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1751

<400> 74  
gtacttgaac tcgttcctg

19

<210> 75  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1857

<400> 75  
ggcaagggca gcagccgg

18

<210> 76  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1823

<400> 76  
agcttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct

53

<210> 77  
<211> 54  
<212> DNA  
<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1829

<400> 77

ctagagaatt cgcggccgct cgaggtaccg gatccatoga tgcgacctg caga 54

<210> 78

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1820

<400> 78

agctctagag attcgcggcc gctcgaggta ccgcatccat cgatgtcgac ctgcagaagc 60

ttg

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctgcaggtc gacatcgatg gatccggtac ctcgagcggc cgcgaattct 60

ctag

64

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 80

caggatccga gtctcaaccc tcaac 25

<210> 81

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1929

<400> 81  
gggaattcct tatcaattct caatctgggg taggcacaac ttc 43

<210> 82  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2452

<400> 82  
cacagtcgac ttacatttgc ttctgacaca actgtgttca ctagcaacct caaacagaca 60  
ccatgggcct ctccaccgtg c 81

<210> 83  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1922

<400> 83  
gaggctgcaa ttgaagc 17

<210> 84  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2316

<400> 84  
attcgtgcgg cgcctag 17

<210> 85  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-2467

<400> 85  
gtcggtagca ccaagga

17

<210> 86  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 86  
gttttcccag tcacgac

17

<210> 87  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer EBI-2112

<400> 87  
gtccaattat gtcacacc

18